EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2678	(circular near10 (array or microarray)) same (make or making or made)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:18
L2	1393	(circular near10 (array or microarray)) same construct$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:18
L3	160	(circular near10 (array or microarray)) same synthesi$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:18
L4	147	(circular near10 (array or microarray)) same bind$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:18
L5	110	(circular near10 (array or microarray)) same bound	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:18
L6	1621	(circular near10 (array or microarray)) same attach$	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:49
L7	5240	l1 or l2 or l3 or l4 or l5 or l6	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:19
L8	1264980	@rlad<"20030725"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:19
L9	1749	l7 and l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:31

6/16/07

EAST Search History

L10	40928	435/6[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:32
L11	529	435/91.4[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:32
L12	734	435/91.41[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:32
L13	35639	435/320.1[ccls]	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:32
L14	68091	l10 or l11 or l12 or l13	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:32
L15	95	l9 and l14	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:40
L16	1465	(circular near10 (array or microarray)) same (produce producing)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:49
L17	166	l9 and l16	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:50
L18	10	l14 and l17	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:50
L19	0	l18 not l15	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:54

EAST Search History

L20	447	l16 and l8	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:54
L21	102998	l14 an dl20	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:54
L22	14	l14 and l20	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:54
L23	9	l22 not l6	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/06/16 12:54

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NEWS 3 JAN 16 CA/CAplus Company Name Thesaurus enhanced and reloaded
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NEWS 22 MAR 30 RDISCLOSURE reloaded with enhancements
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NEWS 24 APR 30 GENBANK reloaded and enhanced with Genome Project ID field
NEWS 25 APR 30 CHEMCATS enhanced with 1.2 million new records
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NEWS 28 MAY 01 New CAS web site launched
NEWS 29 MAY 08 CA/CAplus Indian patent publication number format defined
NEWS 30 MAY 14 RDISCLOSURE on STN Easy enhanced with new search and display fields
NEWS 31 MAY 21 BIOSIS reloaded and enhanced with archival data
NEWS 32 MAY 21 TOXCENTER enhanced with BIOSIS reload
NEWS 33 MAY 21 CA/CAplus enhanced with additional kind codes for German patents
NEWS 34 MAY 22 CA/CAplus enhanced with IPC reclassification in Japanese patents

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1337575 SINGLE/BI 1248442 SINGLE/AB
140354 STRAND?/BI 121307 STRAND?/AB
28700 SS/BI 26376 SS/AB 3811
SSDNA#/BI 3142 SSDNA#/AB

6/16/07

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L2 207025 (ARRAY? OR MICROARRAY?)/BI,AB

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L3 24 L1 AND L2

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=> s l4 not 2006/py 1440503 2006/PY
L5 16 L4 NOT 2006/PY

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L6 12 L5 NOT 2005/PY

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L7 7 L6 NOT 2004/PY

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L4 20 S L3 NOT 2007/PY
L5 16 S L4 NOT 2006/PY
L6 12 S L5 NOT 2005/PY
L7 7 S L6 NOT 2004/PY

=> d l7 1-7 bib ab

L7 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2002:404132 CAPLUS <<LOGINID::20070616>>
DN 137:363719
TI Super DNA material
AU Sugimoto, Naoki; Okumoto, Yasuhide
CS Department of Science and Engineering, Konan University, Japan
SO Mirai Zairyo (2002), 2(4), 22-29 CODEN: MZIABA
PB Enu-Ti-Esu
DT Journal; General Review
LA Japanese
AB A review. The use of DNA and RNA mols. with structural uniqueness as material resource was discussed. Ribozymes, RNA prodn. by rolling synchronization of RNA polymn. by using ***single*** - ***stranded*** ***circular*** DNAs, antisense DNAs, DNA ribozymes catalyzing metalation, functional DNA chips with catalytic activities were described as specific examples in which DNAs or RNAs were used as core materials of the system.

L7 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2001:584675 CAPLUS <<LOGINID::20070616>>
DN 136:196899
TI Evidence for a rolling-circle mechanism of phage DNA synthesis from both replicative and integrated forms of CTX.phi.
AU Moyer, Kathryn E.; Kimsey, Harvey H.; Waldor, Matthew K.
CS Howard Hughes Medical Institute, Division of Geographic Medicine and Infectious Diseases, New England Medical Center and Department of Molecular Biology and Microbiology, Tufts University School of Medicine, Boston, MA, 02111, USA
SO Molecular Microbiology (2001), 41(2), 311-323 CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell Science Ltd.
DT Journal
LA English
AB The genes encoding cholera toxin, the principal virulence factor of Vibrio cholerae, are part of the ***circular*** ***single*** - ***stranded*** DNA genome of CTX.phi.. In toxigenic V. cholerae strains, the CTX.phi. genome is typically found in integrated ***arrays*** of tandemly arranged CTX prophages. Infected cells that lack a chromosomal integration site harbor the CTX.phi. genome as a plasmid (pCTX). We studied the replication of pCTX and found several indications that this plasmid replicates via a rolling-circle (RC) mechanism. The initiation and termination sites for pCTX plus-strand DNA synthesis were mapped to a 22bp sequence that contains inverted repeats and a nonanucleotide motif found in the plus-strand origins of several RC replicons. Furthermore, similar to other RC replicons, replication of plasmids contg. duplicated pCTX origins resulted in the deletion of sequences between the two origins and the formation of a single chimeric origin. Our previous work revealed that CTX prophage ***arrays*** give rise to hybrid CTX virions that contain sequences derived from two adjacent prophages. We now report that the boundaries between the sequences contributed to virions by the upstream and the downstream prophages in an ***array*** correspond to the site at which synthesis of plus-strand pCTX DNA is initiated and terminated. These data support the model that plus-strand CTX.phi. DNA is generated from chromosomal prophages via a novel process analogous to RC replication.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1999:529954 CAPLUS <<LOGINID::20070616>>
DN 131:295992
TI Structural analysis of adeno-associated virus transduction circular intermediates
AU Duan, Dongsheng; Yan, Ziying; Yue, Yongping; Engelhardt, John F.
CS Department of Anatomy and Cell Biology and Department of Internal Medicine, The University of Iowa, Iowa City, IA, 52242, USA
SO Virology (1999), 261(1), 8-14 CODEN: VIRLAX; ISSN: 0042-6822
PB Academic Press
DT Journal
LA English
AB Recombinant adeno-assocd. virus (rAAV) has recently been demonstrated to form circular intermediates following transduction in muscle tissue and cell lines. Although restriction enzyme and Southern blot anal. has revealed a consistent monomer and multimer head-to-tail conformation, detailed structural sequence anal. has been lacking due to the high secondary structure of the ITR ***arrays*** . To gain further insight into potential mechanisms by which AAV ***circular*** genomes are formed from linear ***single*** - ***stranded*** viral DNA, we have performed chem. sequencing of ITR ***arrays*** within seven circular intermediates independently isolated from primary fibroblasts and Hela cells. Results from these studies demonstrated several types of circular intermediates with mosaic ITR elements flanked by two D sequences. The most predominant form consisted of a

structure similar to that of previously generated AAV double-D plasmids, with one complete ITR flanked by two D-region elements. However, intermediately deleted ITR ***arrays*** with more than one complete ITR were also seen. Based on this structural information, we have proposed a model for formation of AAV ***circular*** intermediates by recombination/ligation between ITR ends of panhandle ***single*** - ***stranded*** AAV genomes. (c) 1999 Academic Press.
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1995:311260 CAPLUS <<LOGINID::20070616>>
DN 122:76335
TI Matching electrostatic charge between DNA and coat protein in filamentous bacteriophage. Fiber diffraction of charge-deletion mutants
AU Symmons, Martyn F.; Welsh, Liam C.; Nave, Colin; Marvin, Don A.; Perham, Richard N.
CS Cambridge Centre Molecular Recognition, Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SO Journal of Molecular Biology (1995), 245(2), 86-91 CODEN: JMOBAK; ISSN: 0022-2836
PB Academic
DT Journal
LA English
AB The virion of the Ff (fd, f1, M13) filamentous bacteriophage consists of a long tube of coat protein subunits in a shingled, helical ***array*** , surrounding a genome of ***circular*** ***single*** - ***stranded*** DNA. Modified fd virions have been generated by a mutation (K48A) that removes one pos. charge from each coat protein subunit in the C-terminal region of the polypeptide chain facing the DNA. The no. of nucleotides in the mutant DNA is unchanged, but the K48A virions are 35% longer than the wild type. The authors measured the X-ray diffraction attributable to single virions in hydrated gels of wild-type and K48A bacteriophages. Most of the diffraction pattern shows no significant difference between wild-type and K48A. Since the DNA is only about 12% different by wt. of the wild-type virion, the diffraction pattern is dominated by the protein contribution, and the absence of significant differences indicates that there are no significant changes in the symmetry or structure of the protein coat. But there is a change in the diffraction pattern in a region where the DNA and protein contributions are comparable. The diffraction pattern of the K48A mutant shows an increase in intensity of one of the weaker equatorial peaks, relative to the wild type, in a region where the protein contribution has a neg. sign but the DNA contribution has a pos. sign. This is consistent with a decrease in the ratio of DNA:protein per unit length of the K48A mutant. The results suggest that the protein forms a sheath lined with pos. charges interacting electrostatically and non-specifically with a neg. charged DNA core of matching charge d. The lower pos. charge d. lining the capsid in the K48A mutant means that correspondingly fewer nucleotides can be packaged per coat protein subunit, which in turn requires an elongation of the DNA inside the virion. A longer virion is thus required to package the same amt. of DNA. Within the error of measurement, the no. of pos. charges on the protein interacting with the DNA is the same in K48A as in the wild type, despite the fact that the mutant is 35% longer than the wild type.

L7 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1992:441796 CAPLUS <<LOGINID::20070616>>
DN 117:41796
TI Cell-free system for assembly of transcriptionally repressed chromatin from Drosophila embryos
AU Becker, Peter B.; Wu, Carl
CS Lab. Biochem., Natl. Cancer Inst., Bethesda, MD, 20892, USA
SO Molecular and Cellular Biology (1992), 12(5), 2241-9 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB A cell-free system was derived from preblastoderm Drosophila embryos, for the efficient assembly of cloned DNA into chromatin is described. The chromatin assembly system utilizes endogenous core histones and assembly factors and yields long ***arrays*** of regularly spaced nucleosomes with a repeat length of 180 bp. The assembly system is also capable of complementary-strand DNA synthesis accompanied by rapid nucleosome formation when the starting template is ***single*** - ***stranded*** ***circular*** DNA. Chromatin assembled with the preblastoderm embryo ext. is naturally deficient in histone H1, but exogenous H1 can be incorporated during nucleosome assembly in vitro. Regular spacing of nucleosomes with or without histone H1 is sufficient to maximally repress transcription from hsp70 and fushi tarazu gene promoters. The Drosophila assembly system should be particularly useful for in vitro studies of chromatin assembly during DNA synthesis and for elucidating the action of transcription factors in the context of native chromatin.

L7 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN
AN 1987:420459 CAPLUS <<LOGINID::20070616>>
DN 107:20459
TI Interactions between DNA and coat protein in the structure and assembly of filamentous bacteriophage fd
AU Hunter, Gary J.; Rowitch, David H.; Perham, Richard N.
CS Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SO Nature (London, United Kingdom) (1987), 327(6119), 252-4 CODEN: NATUAS; ISSN: 0028-0836
DT Journal
LA English
AB Bacteriophage fd is a class I filamentous virus that comprises a ***circular*** , ***single*** - ***stranded*** DNA mol. enclosed in a cylindrical protein sheath to form a flexible particle .apprx.890 nm long and 7 nm in diam. The viral DNA contains 6408 nucleotides incorporating 10 genes, and the protein sheath is composed of .apprx.2700 major coat protein subunits in a shingled helical ***array*** , the symmetry of which is defined by a 5-fold rotational axis combined with a 2-fold screw axis of pitch 3.2 nm. The DNA extends throughout the length of the particle but is not base-paired and has a symmetry different from that of the protein helix. How the DNA is packed remains unclear, but the no. (2.4) of nucleotides packaged per major coat protein subunit is certainly not integral, in contrast with, say, the packaging of RNA in tobacco mosaic virus. The coat protein subunit is 50 amino acid residues in length and, in the virus particle, adopts a largely .alpha.-helical conformation, with the long axis of the helix aligned close to the long axis of the filament. This protein is arranged with its neg. charged N-terminal region on the outside of the filament and its pos. charged C-terminal region on the inside abutting the DNA. A pos. charge on 1 of the 4 lysine side-chains in the latter region has a direct effect on DNA packaging, because when this charge is absent, elongated particles are produced with lengths that can be correlated with the residual pos. charge in the C-terminal region of the coat protein subunit.

L7 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1986:511803 CAPLUS <<LOGINID::20070616>>
DN 105:111803
TI DNA-protein interactions and DNA packaging in filamentous bacteriophages
AU Rowitch, David H.; Hunter, Gary J.; Perham, Richard N.
CS Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SO Biochemical Society Transactions (1986), 14(6), 1168-9
CODEN: BCSTB5; ISSN: 0300-5127
DT Journal
LA English
AB The filamentous phages fd (infecting Escherichia coli) and Pf1 (infecting Pseudomonas aeruginosa) have genomes of ***circular*** , ***single*** - ***stranded*** DNA surrounded by a tubular ***array*** of .alpha.-helical coat protein subunits. The process of phage assembly is essentially the same in the 2 viruses. An obvious difference between the fd and Pf1 coat proteins is in the clustering of pos. charged side chains (lysine and arginine residues) in the C-terminal regions. The lysine at position 48 of the C-terminus of the fd coat protein was successfully mutated to arginine and glutamine, demonstrating that a pos. charge at this site is not essential for phage assembly. Genetic engineering expts. showed that the Pf1 coat protein could not be used efficiently in fd virion assembly.

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L2 207025 S (ARRAY? OR MICROARRAY?)/BI,AB
L3 24 S L1 AND L2
L4 20 S L3 NOT 2007/PY
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L7 7 S L6 NOT 2004/PY

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